

Figure S1. Current Consensus of Evolutionary Relationships of Major Lineages within Kingdom Fungi. Related to Figure 1.

Phyla not sampled in this study are shown in red font.

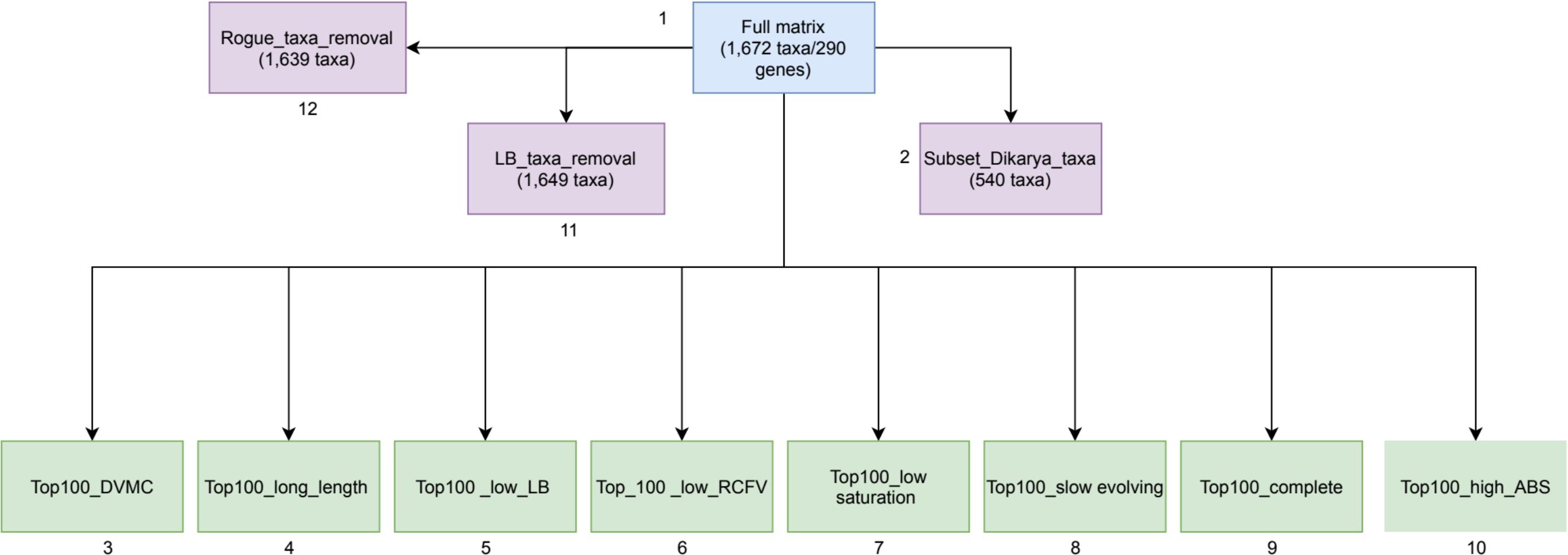


Figure S2. Relationships between the 12 Data Matrices Analyzed in this Study. Related to Figures 2 and 3.

Data matrices with taxon-based filtering are in purple boxes and those with gene-based filtering are in green boxes. The number for each data matrix corresponds to its number in the STAR Methods section. See STAR Methods for further information on each data matrix and filtering strategy used to generate it.

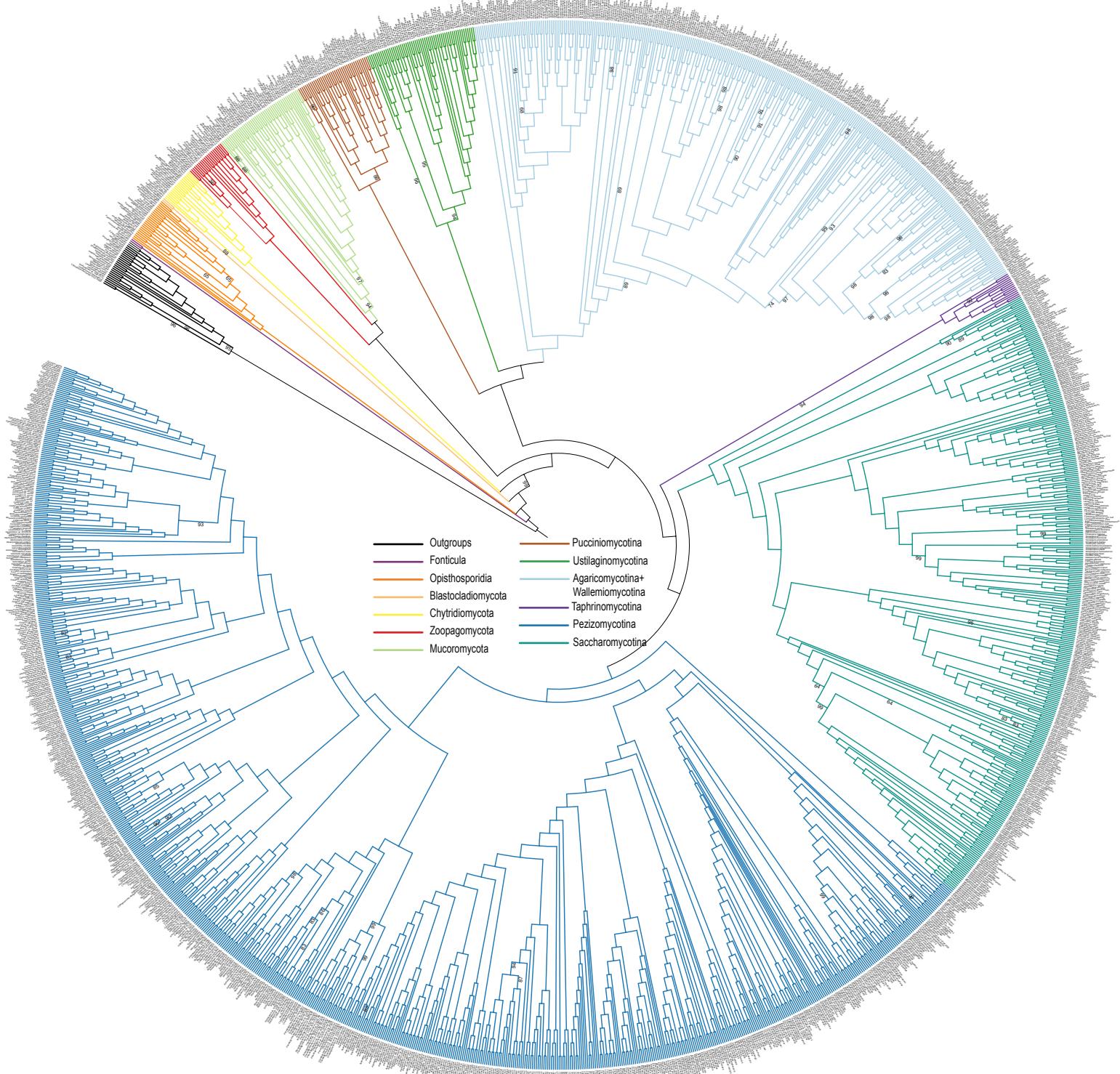


Figure S3. The Genome-scale Phylogeny of 1,644 Species in the Fungal Kingdom.

Related to Figure 2 and Data S1.

The tree of the 1,644 fungal species and 28 outgroups was reconstructed from the maximum likelihood concatenation analysis of 290 single-copy BUSCO genes under a single LG+G4 model ($\ln L = -78287339.984$). All internal branches were supported with 100% ultrafast bootstrap value unless otherwise noted. See also Figure 2 and Data S1.

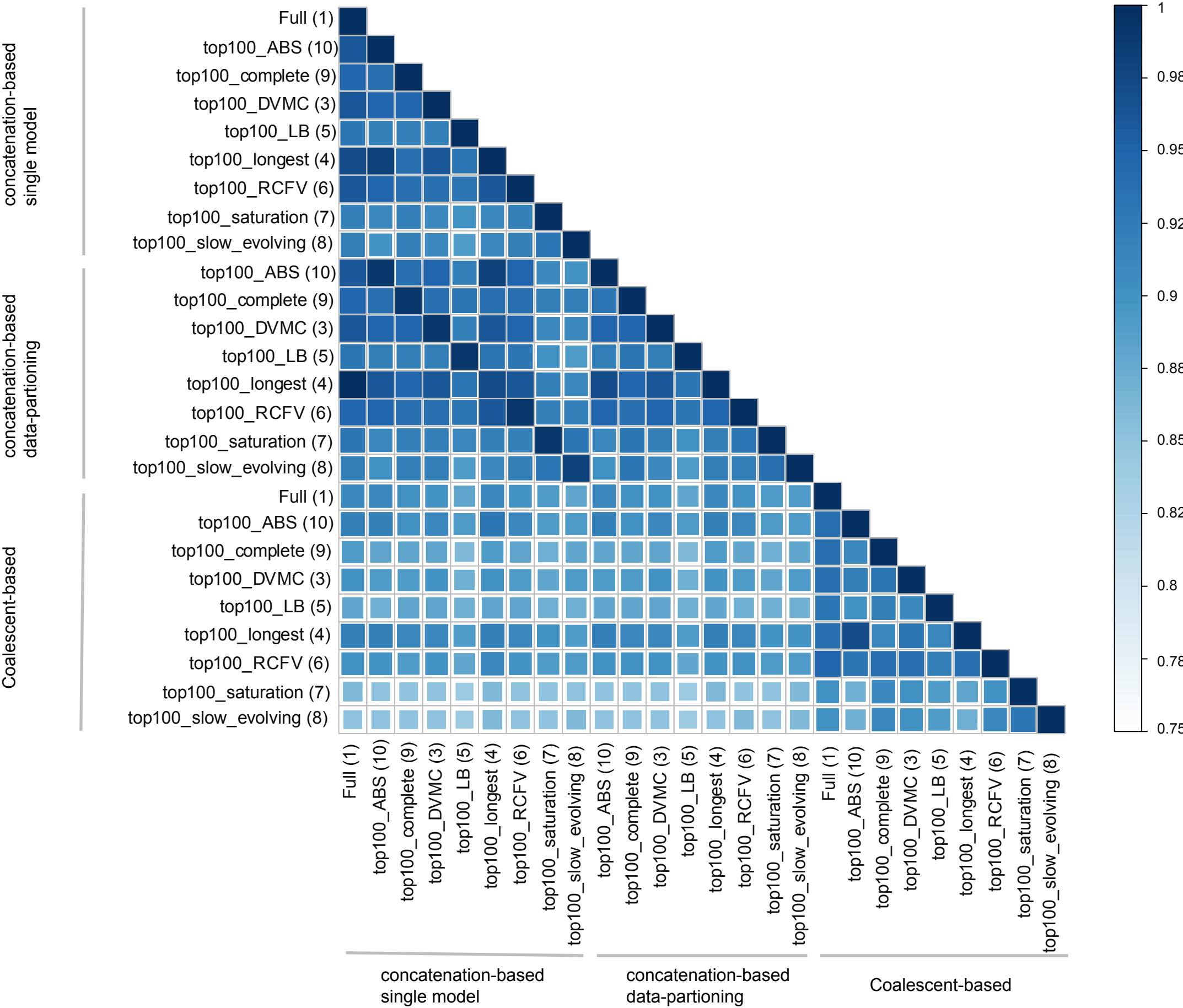
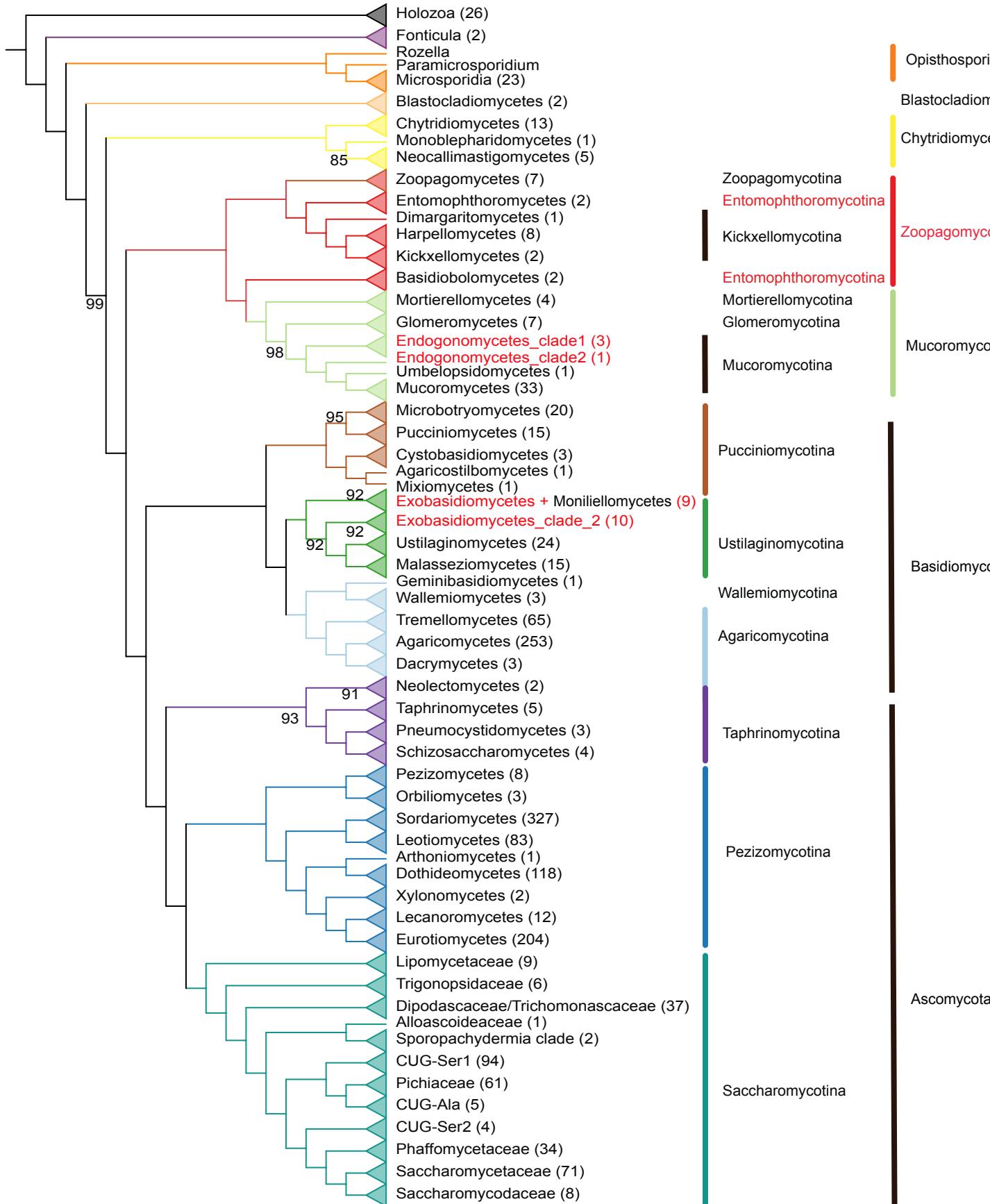


Figure S4. Heatmap of Topological Similarities for All Pairwise Comparisons among the Phylogenies Reconstructed from Analyses of 12 Different Data Matrices Using Three Different Approaches, Include Concatenation Under a Single Partition, Concatenation Under Gene-based Partitioning, and Coalescence. Related to Figure 3.

The topological congruence between each pair of phylogenies was calculated using Gotree. The size and color of the squares represents the degree of congruence as measured by percentage. Results from data matrices 2, 11, and 12 are not shown here since they have different sets of taxa that have been removed.

A Concatenation Tree



B Coalescence Tree

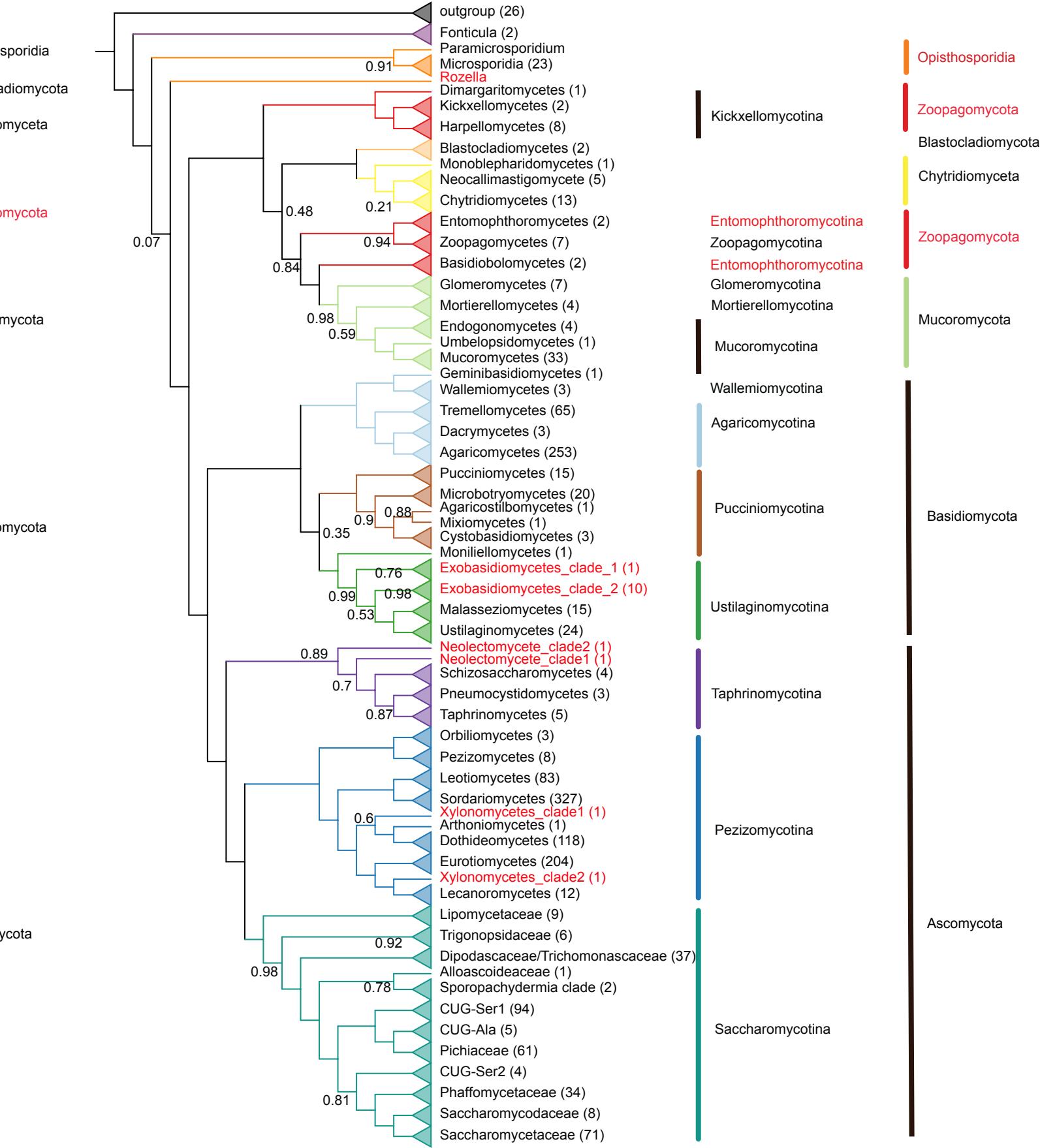


Figure S5. Incongruence between Concatenation- and Coalescent-based Phylogenies of Fungi. Related to Figure 3.

Topologies derived from maximum likelihood analysis using (A) a concatenation single model (LG+G4) approach and (B) a coalescence approach. Numerical values below branches represent (A) ultrafast bootstrap (BS) values and (B) local posterior probabilities (LPP); unlabeled branches received 100% BS or 1.0 PP support. Termini are labeled using major lineages of fungi. Taxa in red correspond to groups inferred to be paraphyletic by the topology shown. Termini are labeled using class-level taxonomic names from NCBI, except for in Saccharomycotina, where informal and family-level names reflecting the 12 major clades comprising this group are used.

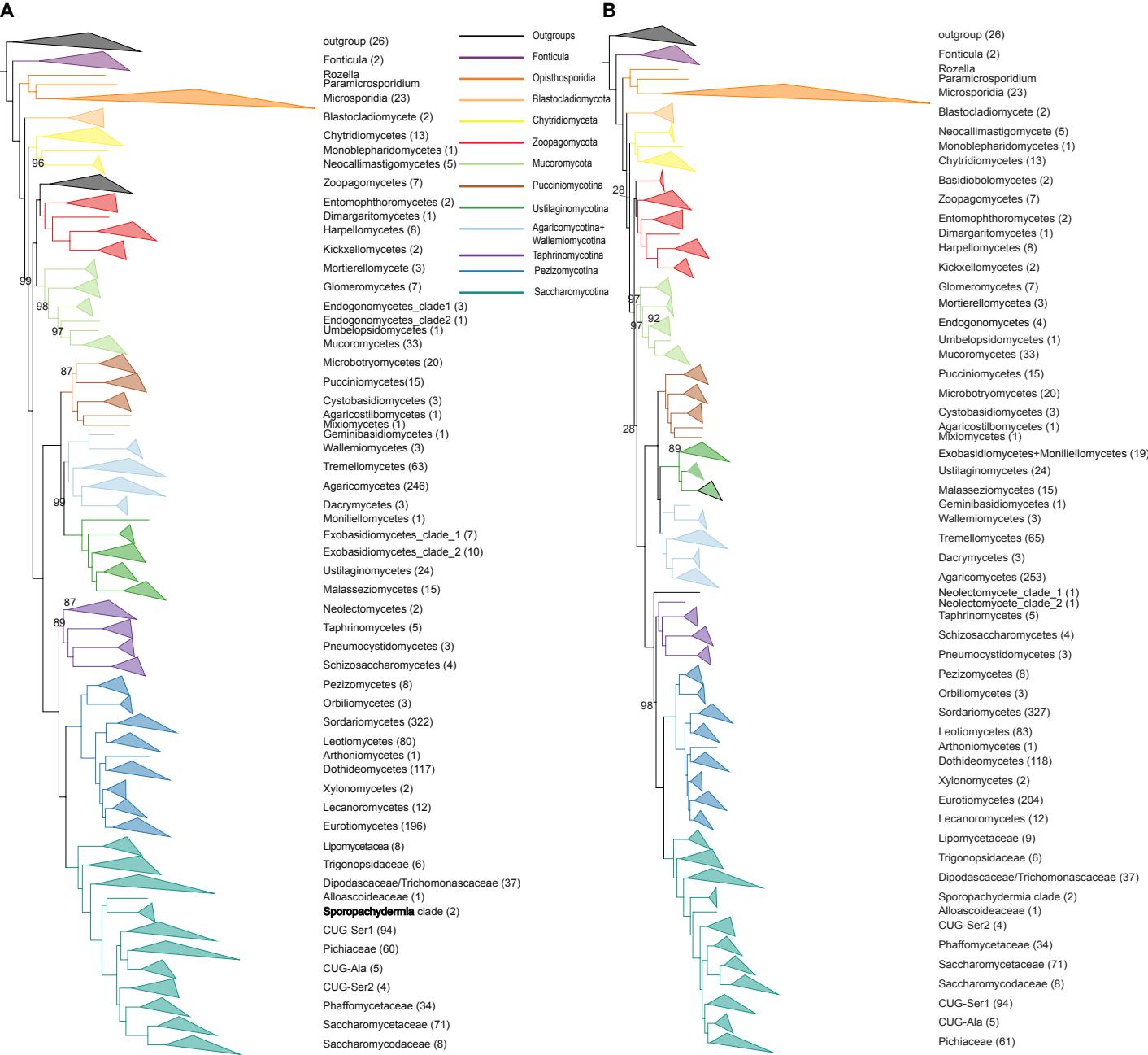


Figure S6. Phylogenetic Hypotheses from the Rogue_taxa_removal and Top100_slow_evolving Data Matrices. Related to Figures 2 and 3.

(A) Phylogeny of 1,639 fungal species from the Rogue_taxa_removal data matrix. The topology shown was obtained from maximum likelihood analysis of a concatenated data matrix of 290 genes under a single LG+G4 model ($\ln L = -76877622.807$). (B) Phylogeny of 1,672 fungal species from the Top100_slow_evolving data matrix under a single LG+G4 model. The topology shown was obtained from maximum likelihood analysis of a concatenated data matrix of 290 genes under a single LG+G4 model ($\ln L = -13426586.414$). All internal branches were supported with 100% ultrafast bootstrap values unless otherwise noted. Termini are labeled using the class-level ranking derived from NCBI taxonomy (except for subphylum Saccharomycotina, where termini are labeled using each one of the 12 major clades to reflect the current understanding of Saccharomycotina phylogeny).